AMENDMENT TO CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

1-27. (Cancelled) .

28. (New) A method for distinguishing AML subtypes with aberrant and prognostically intermediate karyotypes selected from the group consisting of trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1,

wherein

a higher expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 46, 47, 48, 49, and 50, of Table 1, and

a lower expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 18, 41, and 45, of Table 1,

or wherein

a higher expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 46, 47, 48, 49, and 50, of Table 1, or

a lower expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 18, 41, and 45, of Table 1,

is indicative for a specific median event-free survival (EFS) and

29. (New) A method for distinguishing AML subtypes with aberrant and prognostically intermediate karyotypes selected from the group consisting of trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined as defined in Table 2,

wherein

a higher expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 45, 49, and 50 of Table 2, and

a lower expression of at least one polynucleotide defined by any of the numbers 24, 44, 46, 47, and 48, or by any of the numbers 24, 44, 46, 47, or 48 of Table 2

or wherein

a higher expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 46, 47, 48, 49, and 50, of Table 2, or

a lower expression of at least one polynucleotide defined by any of the numbers selected from the group consisting of 18, 41, and 45, of Table 2,

is indicative for a specific median overall survival (OS).

30. (New) The method according to claim 28 or 29 wherein the polynucleotide is labelled.

31. (New) The method according to claim 28 or 29, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

32. (New) The method according to claim 28 or 29, wherein the expression level of at least two, of the markers of at least one of the Tables 1-2 is determined.

33. (New) The method according to claim 28 or 29, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, i.e. 2-fold lower, in the first subtype.

34. (New) The method according to claim 28 or 29, wherein the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, i.e. 2-fold higher in the first subtype.

35. (New) The method according to claim 28 or 29, wherein the sample is from an individual having AML.

36. (New) The method according to claims 28 or 29, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.

37. (New) The method according to claim 36, wherein the transcribed polynucleotide is a mRNA or a cDNA.

38. (New) The method according to claim 36, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.

39. (New) The method according to claim 28 or 29, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

40. (New) The method according to claim 36, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.

41. (New) The method according to claim 40, wherein the compound is an antibody, or a fragment thereof.

42. (New) The method according to claim 28 or 29, wherein the method is carried out on an array.

43. (New) The method according to claim 28 or 29, wherein the method is carried out in a robotics system.

44. (New) The method according claim 28 or 29, wherein the method is carried out using microfluidics.

45. (New) Method for diagnosing AML subtypes with aberrant and prognostically intermediate karyotypes selected from the group consisting of trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), in a sample, the method comprising determining the expression level of

markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in claim 28 or 29.

46. (New) Method according to claim 45 for diagnosing AML subtypes with aberrant and prognostically intermediate karyotypes selected from the group consisting of trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in claim 1 or 2, in an individual having AML.

47. (New) A diagnostic kit containing at least one marker as defined in claim 28 or 29 for distinguishing AML subtypes with aberrant and prognostically intermediate karyotypes selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), or selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), or del(20q), in combination with suitable auxiliaries.

48. (New) The diagnostic kit according to claim 47, wherein the kit contains a reference for the AML subtypes with aberrant and prognostically intermediate karyotypes selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), or selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), or del(20q).

49. (New) The diagnostic kit according to claim 48, wherein the reference is a sample or a data bank.

50. (New) An apparatus for distinguishing AML subtypes with aberrant and prognostically intermediate karyotypes selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q), or selected from trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), or del(20q) in a sample containing a reference data bank.

51. (New) The apparatus according to claim 50, wherein the reference data bank is obtainable by comprising

compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1 or 2, and

classifying the gene expression profile by means of a machine learning algorithm.

52. (New) The apparatus according to claim 51, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.

53. (New) The apparatus according to claim 50, wherein the apparatus contains a control panel or a monitor.

54. (New) A reference data bank for distinguishing AML subtypes with aberrant and prognostically intermediate karyotypes selected from the group consisting of trisomy 8, inv(3), t(3;3), trisomy 11, trisomy 13, trisomy 4, t(1;3), t(6;9), der(5)t(5;11), i(17), del(9q), del(12p), and del(20q) obtainable by comprising

compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in in Tables 1 or 2,

classifying the gene expression profile by means of a machine learning algorithm.

55. (New) The reference data bank according to claim 54, wherein the reference data bank is backed up and/or contained in a computational memory chip.